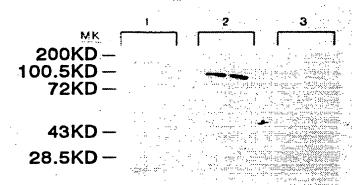


FIGURE 1



1 - anti- EGFr PoAB RK-2 2 - Cyt-356 MoAB/RAM 3 - RAM

PCT/US93/10624

FIGURE 2A

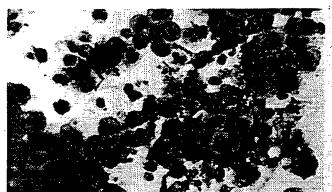


FIGURE 2B

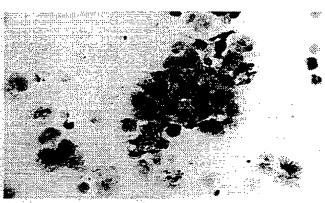


FIGURE 2C

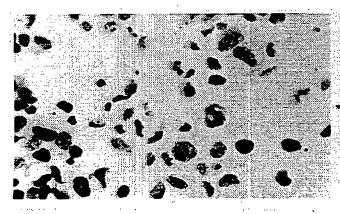


FIGURE 2D

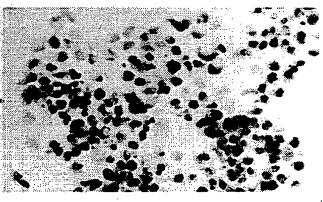


FIGURE 3A







FIGURE 3B

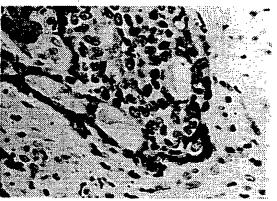


FIGURE 3C

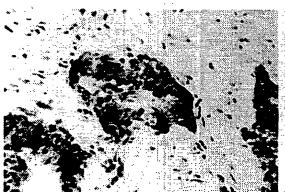
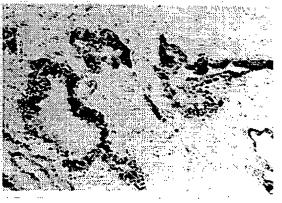


FIGURE 3D



PCT/US93/10624

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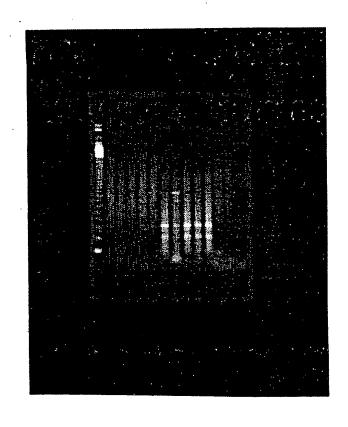
FIGURE 4

100.5

43.0

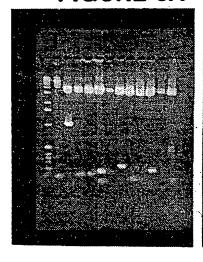
28.5

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FIGURE 6A FIGURE 6B



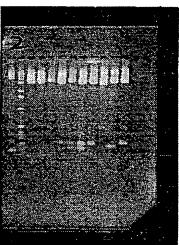


FIGURE 7

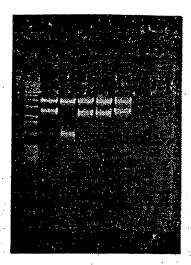
6.1KB →

0.5KB --

PCT/US93/10624

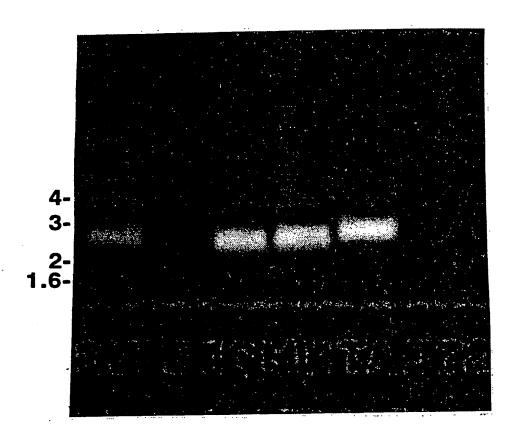
8/48

FIGURE 8

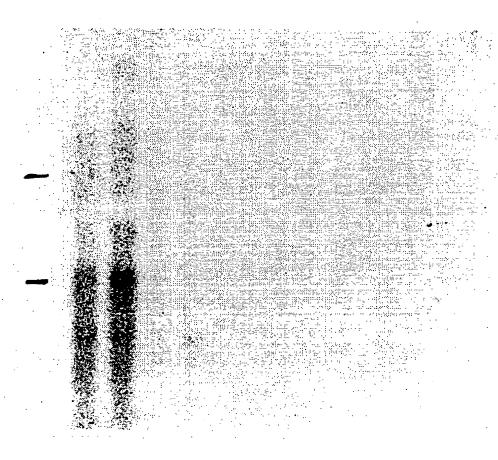


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FIGURE 9



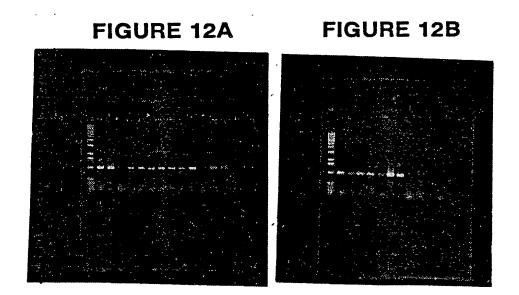
10/48 FIGURE 10



11/48 FIGURE 11

1 2 3 9.5___ 7.5__ 4.4__ 2.4__

12/48



13/48 FIGURE 13

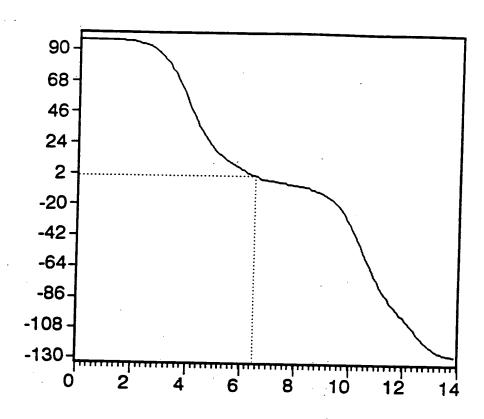


FIGURE 14-1

Done on sequence PMSANTIGEN.
Total number of residues is: 750.
Analysis done on the complete sequence.

8 4 10 **^**|| **∧** î Â AA AA 309 264 16 101 CNAT CNAT CNAT -88 0 II II 11 conformation conformation conformation conformation (E) Extended Helical Turn Coil

14/48

Sequence shown with conformation codes.

given conformation are Ø in or more residues Ŋ of Consecutive stretch overlined

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回	ပ	लि	ि	धि	lE	<u>।</u> ध	धि	াচ্য	ပ	旧	लि	
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91	121	151	181	211	241	271	301	331	361	191	121	

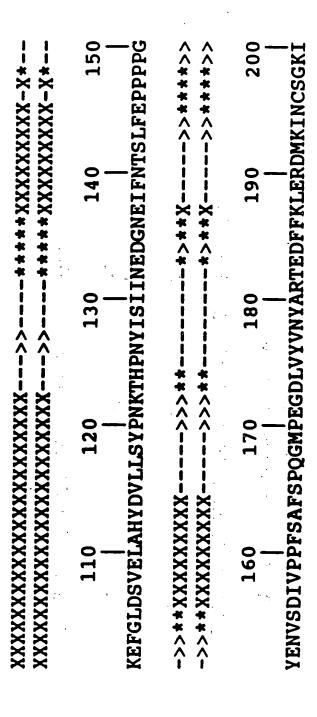
Ħ	旧	H	IH	IH	नि	巨	回	ပ	IH
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Ħ	E	田	II	IH	回	回	नि	IΞ	II
H	E	E	IH	E	旧	ပ	 丘	II	IΞ
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H	H	臼	II	E	 	H	 臼	田	II
H	IO	ध	II	E	IEI	H	E	II	IH
H	10	匝		巨	II	Ħ	E	II	田田
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曰	D	ပ	II	回	H	II	Ö	IH	IH
田	IJ	Ö	II	IH	II	II	Ö	IH	IH
曰	H	H	II	II	IH	II	H	F	IX
凹	H	IH	II	II	ပ	III	H	团	II
臼	H	II	II	II	ပ	IX	团	E	E
团	H	IH	巨	IH	H	IH	曰	E	E
臼	IH		E	旧	回	H	H	E	नि
臼	IH	II	旧	lei	回	田	H	E	F
回	II	ल	E	旧	回	II	H	IEI	旧
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田	H	田	旧	[단	H	IX	H	旧	lei
曰	王	IO	lei	巨	IX	II	II	H	回
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Ħ	II	10	. IE	FI	王	H	I	U	IH
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r U	II		IH	II	IH	王	I	नि	IX
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ন	III ·	E	H	III	IH	IH	回	回	ပ
451	481	511	541	571	601	631	199	591	721

FIGURE 14-4

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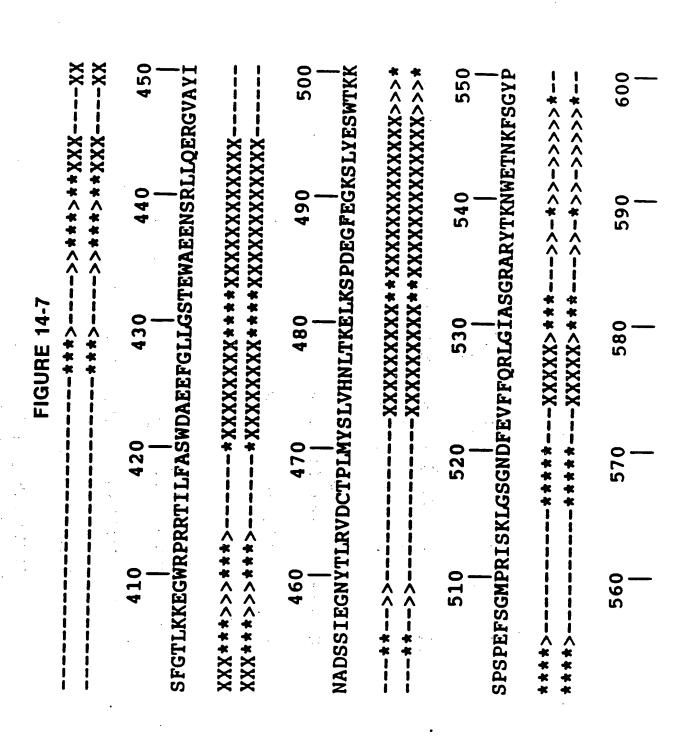
FIGURE 14-5

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1ARYGKVFRGNKVKNAQLAGAKGVILYSDPADYFAPGVKSYPDGWNLPG 1ARYGKVFRGNKVKNAQLAGAKGVILYSDPADYFAPGVKSYPDGWNLPG 260 270 280 290 300	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	14-6 	1 1	**************************************	XX>>>
260 270 280 290 300 300 300 300 300 300 300 300 300 3	210 VIARYGKVFRGNK	220 VKNAQLAGAK	230 GVILYSDPAD	240 YFAPGVKSYPI	250 DGWNLPG
260 270 280 290 300 300	*^^	*XXXXXXXX	^ \	i i	\##-\\\
310 320 330 340 350 350 340 350	260 	270 AGDPLTPGYP	280 ANEYAYRGI	290 AEAVGLPSIPV	300 VHPIGYY
320 330 340 	^^ -	****	XX	# # # # # #	
***>->->->*-**XXXXXX* ***>->>->->	310 AQKLLEKMGGSA	320 PPDSSWRGSLI	330 KVPYNVGPGF	340 GNFSTQKVK	350 HIHSTN
370 380 390	XXXXXXX->>>**	******		-*-*XXXXXX*-*-	* * *
	360	370	380	390	400



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FDCRDY	XXX<	650 	XXXXXX	700 SSHNKY	**** ****	750 	XXXXX
LYHSVYETYELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDY	XXXXX	610 620 630 640 650 AVVLRKYADKIYSISMKHPQEMKTYSVSFDSLFSAVKNFTEIASKFSERL	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	660 670 680 690 700 QDFDKSNPIVLRMMNDQLMCLERAFIDPLGLPDRPFYRHVIYAPSSHNKY		710 720 730 740 750 AGESFPGIYDALFDIESKVDPSKAWGEVKRQIYVAAFTVQAAAETLSEVA	-xxxxxxxxxxxxxx
GMVFEL	XX	LFSAVK	XXXXXX	PDRPFY		IYVAAF	
VAQVRG	x	630 SVSFDS	X	680 IDPLGL	***\\\	730 GEVKRQ	XXXX
FKYHLT	-xxxxx	O - - 	XXXXX**X-	0 CLERAF	XXXXXXXXXXXX>>***>- XXXXXXXXXXXXX>	720 KVDPSKAW	XXXXXXX****XXXXXXX
SKFYDPM	XXXXXX	620 SISMKHPQ	X * * X	670 HMNDQLMC	-XXXXX	7. FDIESK	KXXXXX
ETYELVI	-x-xxxxxxxxxxxxxxxxxxxxxxxxxxxx	610 YADKIY	XXXX	660 NPIVLR	i i	710 GIYDAL	XXX<
LYHSVY		AWLRK	-XXXXXXXXXXX	QDFDKS	**<< <xx< td=""><td>AGESFP</td><td></td></xx<>	AGESFP	
~ .	• •	•		•	- 4 - 4		• •

22/48 FIGURE 15A

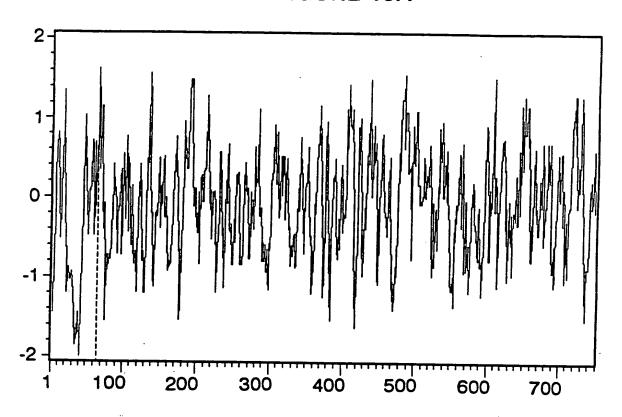


FIGURE 15B

Done on sequence PMSANTIGEN. Total number of residues is: 750. Analysis done on the complete sequence.

-> This is the value recommended by the authors averaging group length is: 6 amino acids. The method used is that of Hopp and Woods. The

The three highest points of hydrophilicity are:

Asp-Glu-Leu-Lys-Ala-Glu Asn-Glu-Asp-Gly-Asn-Glu 68 137 40 to 132 From From 1.57 1.62

482

From

1.55

Lys-Ser-Pro-Asp-Glu-Gly

Ah stands for: Average hydrophilicity.

Note that, on a group of control proteins, only the highest point was in 1001 of the cases assigned to a known antigenic group. The second and third point: proportion of 33% of incorrect predictions. gave a

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~	4	/4	a

		_	10		. 24	/48		
opt	321	311	266	321	æ	£	H • H O	U « 0
initl	120	164	145	120	O CAGGTT	CAGGCT	CAAGTAT:::::CCCACAT	10 ::: :ATGGAGA
initn	203	164	145	203	1070 ICACACC	ACACCC	1130 FGGTCTTCC2 :: :: :: AGGACTACC	1190 AAAATGGGTGG :::::::: AAAATGGATGG
•~			ರ		CHC.	CCTTA 1030	rtgc : :	AAAJ SCAJ
	eptor			eptor	1050 1060 1070 TGGTGCAGGAGCCCTCTCACACCAGGTT	TGGAGACCC	1120 CAGAGGCTGTT :: :: FTGAATCTTCA	1180 AGCTCCTAGA ::: 3GCTGTTCAC
FIGURE 16-1	or transferrin receptor	receptor mRNA, 3' end,	Human transferrin receptor mRNA, complete	for transferrin receptor nt overlap	1020 1030 1040 1050 1060 1070 TGTCCAGCGTGGAATATCCTAAATCTGAATGGTGCAGGAGACCCTCTCACACCAGGTTA	ACATGCCCACCTTGGAACTGGAGACCCTTACACCCCAGGCTT 1010 1020 1030 1040	1080 1090 1100 1110 1120 1130 CCCAGCAAATGAATAGCTTATAGGCGTGGAATTGCAGGGCTGTTGGTCTTCCAAGTAT ::::::::::::::::::::::::::::::::	1140 1150 1160 1170 1180 1190 TCCTGTTCATCCAATTGGATACTATGATGCACAGAAGCTCCTAGAAAAATGGGTGGCTC :::::::::::::::::::::::::::::
FIG	for tran	n recept	rin rece	for transf nt overlap	1040 rcctaaat	GACATGCC 10	1100 CTTATAGG : : :	1160 GATACTAT : : CTAGCAGT
. סאפ		Rať transferrin	cransfer		1030 rggaaata	CCATTCG	1090 FGAATATG	1150 rccaatrg : :: Gaccarct 0
goros	G.qall	Rat tra	Human 1	G.gallus mRNA identity in 717	1020 TGTCCAGCG	CHKTFE TACACTTATCCCATTCGG 990 1000	1080 cccagcaaa7 ::::: cccttcgtt	1140 1150 TCCTGTTCATCCAAT' :::::::: TGCTGTTCAGACCAT' 1110
Tho host	CHKTFER	RATTRFR	HUMTFRR	CHKTFER 51.9%	1 pmsgen T	CHKTFE T	1 pmsgen c : CHKTFE C	pmsgen 1 CHKTFE 1

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1240 1250 CCCTACAATGTTGGACCTGG ::: :: :: TCCTGTAAGGTGACAA 1200 1210	1300 1310 ATCCACTCTACCAATGAAGT : :: :: :: GTGAACAATTCCATGAAAGA 1250 1260	1360 1370 GTGGAACCAGACAGATATGT : :::: : :::: GAAGAACCTGATCGGTATGT 1310 1320	1420 1430 ATTGACCCTCAGAGTGGAGC : : : : : : : : : : : : : : : : : : :
210 1220 1230 1240 1250 ATAGCAGCTGGAGGAAGTCTCAAAGTGCCCTACAATGTTGGACCTGG : :: :::::::::::::::::::::::::::::::	1280	GACAAGAATTTACAATGTGATAGGTACTCTCAGAGGAGCAGTGGAACCAGACAGA	1380 1390 1400 1410 1420 1430 CATTCTGGGAGGTCACCTCATGGGTGTTTGGTGTATTGACCCTCAGAGTGGAGC : :::::::::::::::::::::::::::::::::::
1200 1210 pmsgen AGCACCACCAGATAGCAGC :: :: :: : CHKTFE CACATGCTCTGA-AGGT	1260 CTTTACTGGAAI : ::: : CAAAGCAGGAGA	1320 GACAAGAATTTACAATGTGA : :: :: : CAGGAAGATTCTGAACATCT 1270	1380 1390 CATTCTGGGAGGTCACCGGG : ::::::::::::::::::::::::::::::::
	DIMSGEN CHKTFE (BI) TEEHS ETUTITE BI	pmsgen CHKTFE	pmsgen (CHKTFE

FIGURE 16-3

•	26/4	48	
1490 SAAGGTGGAG : : : : SAGGGCTACAA 1440	1550 CTTCTTGGTTC : :::: SCTGTGGGTGC 1500	1610 SCTTATATTAA :::::::	1620 1640 1650 1670 TGC-TGACTCTATAGAAGGAAACTA-CACTCTGAGATTGATTGTACACCGCTGATG ::::::::::::::::::::::::::::::::::::
1470 1480 149 TGGAACACTGAAAAAGGAAGGGT : : :::::::::::::::::::::::::::::::	1540 AGAATTTGGTC ::::::::::::::::::::::::::::::::	1600 GCGTGGCGTG(: : CCAAAGCTTTC	1660 AGTTGATTGTAC :: : : : SATTTCTGCCAC
1440 1450 1460 1470 1480 1490 AGCTGTTGTTCATGAAATTGTGAG——GAGCTTTGGAACACTGAAAAGGAAGGGTGAG ::::::::::::::::::::::	1500 1510 1520 1530 1540 1550 pmsgen ACCTAGAACTTTTGTTTTGCAAGCTGGGATGCAGAAGTTTTGGTCTTTGTTT :::::::::::::::::::::::	1560 1570 1580 1590 1600 1610 pmsgen TACTGAGTGGCAGAGGAATTCAAGACTCCTTCAAGAGCGTGGCGTGCTTATATTAA :::::::::::::::::::::::::::::	1640 1650 GGAAACTA-CACTCTGAGA(::::::::: GGGAGCAAGCCATGTCAAG(1590 1600
1460 ATTGTGAGG. ::: :::	1520 FGTTTGCAAGC X::::::::	70 1580 GGAGAATTCAAGA ::::X GGGGTACTCTGCC	1640 SAAGGAAACTA ::::::
1450 STTCATGAAAT : ::: FTGTTGGAACT	1510 AGAACAATTTT ::::::::::::::::::::::::::::::	1570 rggcagagga ::: :::: rggcrggaggg	D 1630 CTCATCTATAG : :: : ATGCTCCAGTC 1580
1440 AGCTGTTC :::: TGCTATA1	1500 ACCTAGAAGAACA ::: :: :: ACCGAGGCGAAGC 1450	1560 ::::::::::::::::::::::::::::::::::::	
pmsgen CHKTFE	pmsgen	pmsgen	pmsgen

SUBSTITUTE SHEET (RULE 26)

FIGURE 16-4

27	7/48	
1730 TTTGAAGGC : :: :: TCAGAGAGC 1680	1790 GCATGCCC	GGCCTGGA
1720 3ATGAAGGCT : :::: 3CAGCAGTCT 1670	1780 SAGTTCAGTG	GTTCCTCTT
1710 :::::::::::::::::::::::::::::::::::	1770 CCTTCCCCAG	GACTGGGTAAAGCAGTTGTTCCTCTTG
1700	750 1760 1770 1780 1790 GTTGGACTAAAAAAGTCCTTCCCCAGAGTTCAGTGGCATGCCC	CTTGGCCCAGACTGGGTAAAAGCAGTTGTTCCTCTTGGCCTGGA
1640 CACAACCTAA	1750 176 SAAAGTTGGACTAAAA : : : : : : : :	CAGACTTGGCC 1700
1680 1690 1700 1710 1720 1730 pmsgen TACAGCTTGGTACCTAACAAAAGACCTGAAAAGCCCTGATGAAGGCTTTGAAGGC :::::::::::::::::::::::::::::::::	1740 1 pmsgen AAATCTCTTTATGAAA	CTCTATAACAGA 1690
Dmsgen CHKTFE	pmsgen	CHKTFE
SUBSTITUTE SI	HEET (RULE	26)

IGURE 16-5

164 164 31	CTGGCTT-	ratagat tc	1310 CCAATG :::: ACAATGTACT 0
164	1250 CAATGTTGGAC	CTAGTTGGAAT 660	CACTCT-ACC ::::::::
1, 3' end.	1240 1250 AAAGTGCCCTACAATGTTGGACCTGGC	AACTGTCCTCC 650	1280 1290 1300 1310 TTCTACACAAAAGATGCACATC-CACTCT-ACCAATG ::::::::::::::::::::::::::::::::
errin receptor mRNA, 3' end 560 nt overlap	1230 GAAGTCTCAA	atggaaggaa 640	AAAAGTCAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
<u> </u>	1210 1230 1240 1250 pmsgen ccaccagatagcagcagagagagagagagagagagagaga	RATTRF TGCAGAAAACTTCAAAAACATGGAAACTGTCCTCCTAGTTGGAATATAGATTC 610 620 630 640 650 650	1260 1270 1280 1290 1300 1310 pmsgen -TACTGGAAACTTTTCTACACAAAAGTCAAGATGCACATC-CACTCT-ACCAATG- : :: :: : : : : : : : : : : : : : : :
TTRFR Rat transf 55.5% identity in	1210 ACCAGATAGO	CAGAAAAGCT 620	1260 1270 pmsgen -TACTGGAAACTT : :: :: RATTRF CTCATGTAAGCTG
RATTRFR 55.5% i			1260 Spmsgen -TR RATTRF CTC 670
	JJJJIII	TE STILE!	(11011 20)

FIGURE 16-6

	29/	48	
1370 CAGACAG :::::	1430 CTCAGAG ::::	1480 -AAAAGGAA ::: :: TCAAAAGAT 00	40 rggrcrr :::::
1360 AGTGGAAC : :::: TGAGGAAC 780	1420 TATTGACC: :: TTGCGAAG	14 CTGAA ::: ATGATTTC 900	1540 GAAGAATTTG : : : : : : : : : : : : : : : : : : :
1320 1330 1340 1350 1360 1370 pmsgenAAGTGACAAGTTTTACAATGTGATAGGTACTCTCAGAGGAGCAGTGGAACCAGACAG :::::::::::::::::::::::::::	1380 1390 1400 1410 1420 1430 pmsgen ATATGTCATTGGGAGGTCACCGGGACTCATGGGTGTTTGGTGTATTGACCCTCAGAG ::::::::::::::::::::::::::::::::::	pmsgen T-GGAGCAGCTGTTCATGAAATTGTGAGGAGCTTTGGAACA-CTGAAAAAGGAA : :::::::::::::::::::::::::::::	1490 1510 1520 1540 GGGTGGAGCTTAGAACAATTTTGTTTTGCAAGCTGGGATGCAGAAGAATTTTGTTTTTTTT
340 AGGTACTCTC :: : : TGGCGTTATT 760	TCATGGGTG: 1:::::::::::::::::::::::::::::::	60 AGGAGCTT :::: CCAAGTAT 880	1520 TGCAAGCT::::TGCCAGCT
1340 TGTGATAGG : :: CATCTTTGG	1400 CCGGGACTC : :::: GAGAGACGC	150 1460 ATGAAATTGTGAGG :::::: FTGAAACTTGCCCA 870 88	1510 AATTTTGTT :::::: TATTATCTT 930
1330 ATTTACAAT :: :: ATACTTAAC	1390 3GAGGTCACC ::::::::::::::::::::::::::::::::::	1450 rgttcatgaaz : :::: r-ctgttgaaz	AAGAACA ::: SCAGGAGT
1320 FGACAAGA :::::	1380 pmsgen ATATGTCATTCTGGG ::::::::::::::::::::::::::::::::	1440 GGAGCAGCTGTT ::::::: GGAACAGGTCTT	1490 1500 GGGTGGAGACCTAGAA :: X:::: :: GGATTTAGACCCAGCA
enAAG] ::: R GAAAG! 730	n ATATGTC:::::::::::::::::::::::::::::::::	T-GGAC : :: TGGGAA	
pmsgen RATTRF			pmsgen RATTRF
	Substitute Si	HEET (RULE 26)	

FIGURE 16-7

1550 1560 1570 1580 1590 1600 CTTGGTTCTACTGAGTGGCAGAGAATTCAAGACTCCTTCAAGAGCGTGGCGTG	1610 1620 1630 1640 1650 1660 GCTTATATTAATGCTGACTCTATAGAAGGAAACTA-CACTCTGAGAGTTGATTGTAC ::::::::::::::::::::::::::::::::::::	pmsgen ACCGCTGATGTACAGCTTGGTACCAACCTAACAAAAGACCTGAAAAGC-CCTGATGAAG :::::::::::::::::::::::::::::::
1550 1560 1570 pmsgen ctrggttctactgagtgggcagagaa- :::::::::::::::::::X RATTRF GTTGGTCCGACTGAGTGGCTGGAGGGGTAC 970 980 990	1610 1620 pmsgen GCTTATTTAATGCTGACTCAT :::::::::::::::::::::::::::::::::	1670 1680 pmsgen ACCGCTGATGTACAGCTTGGTAC ::::::::::::::::::::::::::::::::::::
	SHEET (RULE 26)	pms

IGURE 16-8

					31/4	48		
1770	pmsgen GCTTTGAAGGCAAATCTCTTTAT-GAAAGTTGGACTAAAAAAAAGTCCTTCCCCAG		TTGATGGAAAATATCTATATCGAAACAGTAATTGGATTAGCAAAATTGAGGAACTTT	1190	1830	pmsgen AGTTCAGTGGCATGCCCAGGATAAGCAAATTGGGATCTGGAAATGATTTTGAGGTGTTCT	RATTRF CCTTGGACAATGCTGCATTCCCTTTTCTTGCATATTCAGGAATCCCAGCAGTTTCTTTC	1250
1760	CTAAAAAAAG		TTAGCAAAAT	1180	1820	GAAATGATTT	GAATCCCAGC	1240
1750	AGTTGGA	••	AGTAATTGGA	1170	1810	TTGGGATCTG	GCATATTCAG	1230
O	TTAT-GAA	•••	ATATCGAAAC	1160	1800	GATAAGCAAA	CCCTTTTCTT	1220
0 1740	GCAAATCTCT	•••	GAAAATATCT	1150	1790	GCATGCCCAG	ATGCTGCATT	1210
1730	GCTTTGAAG	••	i	1140	1780	AGTTCAGTG	CCTTGGACA	1200
	pmsgen	i	2 RATTRF	IDCT	TITE			1 . .
			Si	IKS [111111	VHFF	. 1 (12)	ı 🕨 '

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-IGURE 16-9

266 145 145 Human transferrin receptor mRNA, complete cd identity in 464 nt overlap 54.3% HUMTFRR

1230 1240 1250 1260 1270 pmsgen AGGAAGTCTCAAAGTGCCTACAATGTTGGACCTGGCTTTAC-TGGAAACTTTTCTACAC : : : : : : : : : : : : : : : : : : :	1300 1310 1320 1330 GCACATC-CACTCT-ACCAATGAAGTGACAAGAATTTACAA : :::::::::::::::::::::::::::::::::
1250 1260 AATGTTGGACCTGGCTTT : : : : : : : : : : : : : : : : : :	1300 1310 ACATC-CACTCT-ACCAATG GAAGCTCACTGTGAGCAATGTGCT 1220 1230
1230 1240 AAGTCTCAAAGTGCCCTACA GGAAGGAGACTGTCCCTCTG 1150 1160	1290 1300 TCAAGATGCACATC-CACT : :: : ::: CAAGAATGTGAAGCTCACT 1210 1220
pmsgen AGGAAG HUMTFR TATGGAA	pmsgen AAAAAGTCAAGATG pmsgen AAAAAGTCAAGATG humtfr AGAAAGCAAGAATG

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pmsgen ccgccactcarccrrrccrccrcarccrcacact-ccacccrcacact HUMTFR GAGAGATGCATGGGGCCCTGGAGCTGCAAAATC-CGGTGTAGGCACAGCTCTCCTATTGA 1430 1420 1400

1500 CCTAGAAGAACAA ::::::: CCCAGCAGAAGCA 1430	1560 TGAGTGGGCAG :::::: TGAATGGCTAG 1490	1620 TGACTCATCT :: :: GGATAAAGCG 1550	1680 GCTTGGT-AC :::: :: GCTTATTGAG 1610
GAGACCTA ::: TCAGCCCA	1550 1560 TTGGTTCTACTGAGTGGG :::::::::::::::::::::::::::::::	0 TTAATGCT:::X TTAATCTG	O TGTACA-G::::: TGTATACGO
480 1490 AAAAGGAAGGGTG ::: X::: TAAAAGATGGGTT	1550 TCTTCTTGG :::: ATCGGTTGG	1610 FGGCTTATAT:::::: FCACTTATAT	1670 CACCGCTGATO :: :: :
1480 ACTGAAAAA : ::: GGTCTTAAA	1540 AGAATTTGG ::::::: AGACTTTGG	1600 AGCGTGGCG : FAAAGGCTTT	1650 1660 1670 168 ************************************
1470 :: : : CTCAGATAT	1530 1540 1550 1560 TGGGATGCAGAATTTGGTCTTCTTGGTTCTGAGTGGCAG ::::::::::::::::::::::::::::::::::	1590 1600 1610 1620 ACTCCTTCAAGAGCGTGGCGTGGCTTATTAATGCTGACTCATCT : ::::X :: :: TC-CCTGCATTTAAAGGCTTTCACTTATTAATCTGGATAAAGCG	1650 1660 1670 1680 CACTCTGAGAGTTGATTGTACACCGCTGATGTACA-GCTTGGT-AC :: ::::::::::::::::::::::::::::::::::
1460 1470 1480 1500 pmsgen AAATTGTGAGGAGCTTTGGAACACTGAAAAAGGAAGGGTGGAGACCTAGAAGAACAA :::::::::::::::::::::::::::::	1510 1520 1530 1540 1550 1560 pmsgen TTTTGTTTGCAAGCTGGGATGCAGAATTTGGTCTTCTTGGTTCTACTGAGGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGAATTTGGTTCTTACTGAGTGGCAGCAGCAGCAGAGAATTTGGATCGGTTGGAGTGGCTAGATTGGAGACTTTGGAGTGCTAGATTGGAGACTTTGGAGAGACTTTGGATTGGAGAGAGA	1570 1580 1590 1600 1610 1620 pmsgen A-GGAGAATTCAAGACTCCTTCAAGAGCGTGGCGTGGCTTATTATTAATGCTGACTCATCT : ::::::::::::::::::::::::::::::::::	1630 1640 1680 ATAGAAGGAAACTACACTCTGAGGTTGATTGTACACCGCTGATGTACA-GCTTGGT-AC : : : : : : : : : : : : : : : : : : :
AAATTG ::::: AACTTG 1380	1510 n TTTTGT' :: : : R TTATCT' 1440	1570 A-GGAGA : :: 3 AGGGATA	1630 ATAGAAG : GTTCTTG
pmsgen HUMTFR			pmsgen HUMTFR
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FIGURE 16-11

34/48 pmsgen ACAACCTAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTTGAAGGCAAATCTTTATG AAAACAATGCAAAATGTGAAGCATCCGGTTACTGGGCAATTTCTATATCAGGACAGCAAC 1670 1660 1650 1640 1700 HUMTFR

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35/48 FIGURE 17A

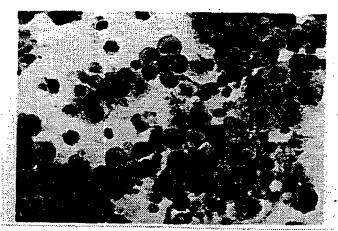


FIGURE 17B

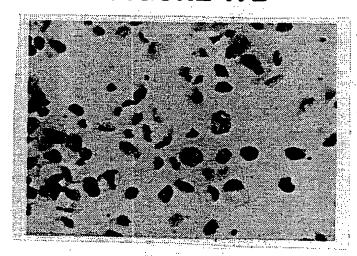
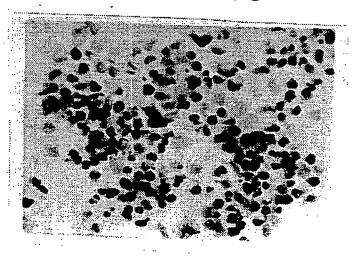


FIGURE 17C



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PCT/US93/10624

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FIGURE 18

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FIGURE 19

1 2 3 4

200 kDa ----

100 kDa ---

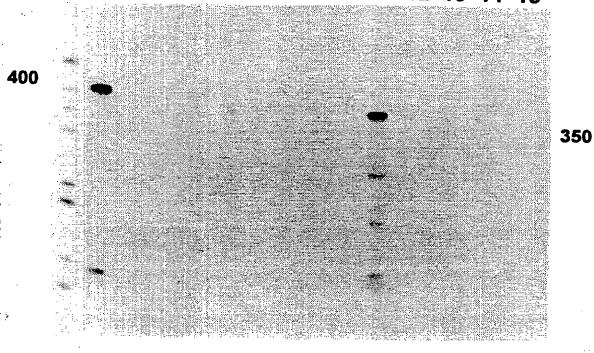
69 kDa ----

--- PSM

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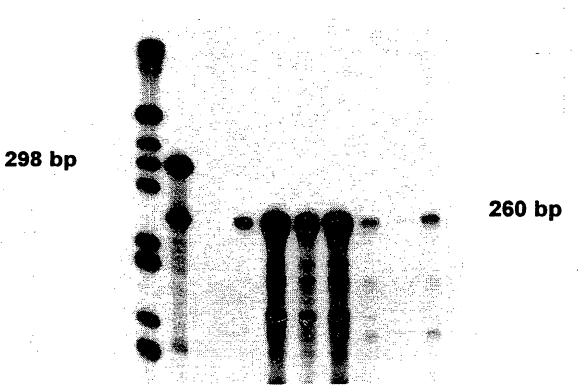
FIGURE 20

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15



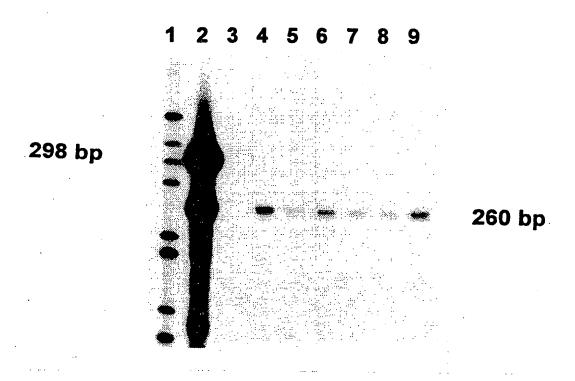
39/48 FIGURE 21

1 2 3 4 5 6 7 8 9 10



PCT/US93/10624

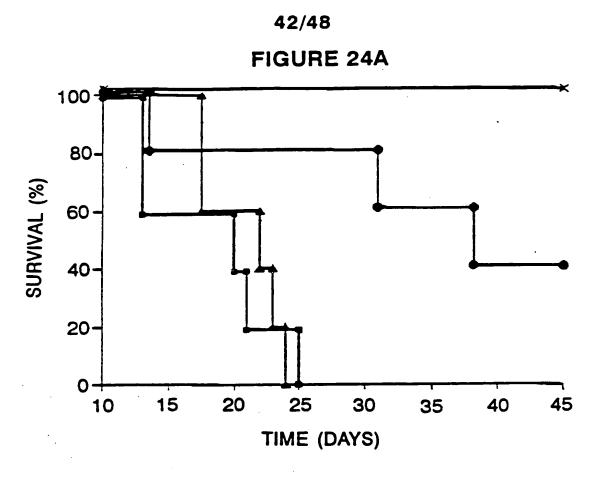
40/48

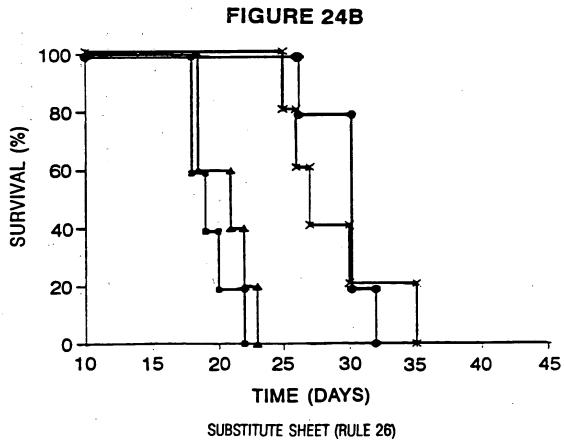


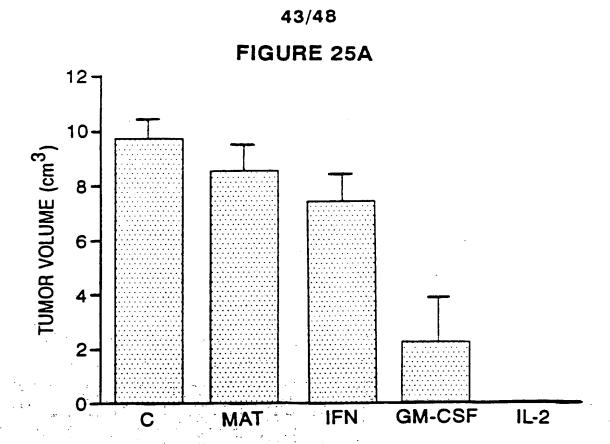
41/48 FIGURE 23

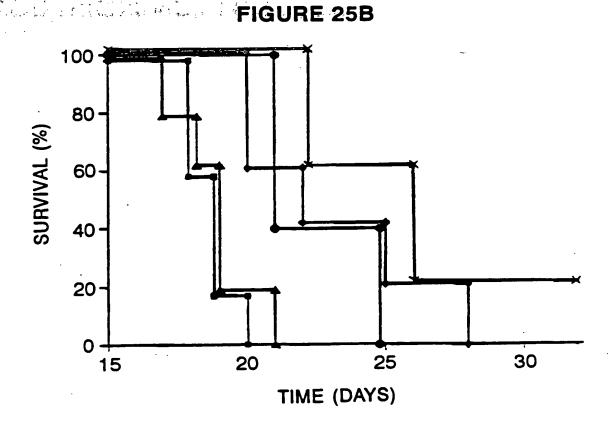
CELL LINE/TYPE	11p11.2-13 REGION	METASTATIC	PSM RNA DETECTED	PSM DNA DETECTED
LNCap			++	ND
HUMAN PROSTATE			++	ND
A9 (FIBROSARCOMA)	NO	NO	· -	-
A9(11) (A9+HUM. 11)	YES	NO	-	REPEAT
AT6.1 (RAT PROSTATE)	NO	YES	-	-
AT6.1-11-c11	YES	NO	+	++
AT6.1-11-c12	NO	YES		-
R1564 (RAT MAMMARY)	NO	YES	_	-
R1564-11-c14	YES	YES	-	+
R1564-11-c15	YES	YES	-	REPEAT
R1564-11-c16	YES	YES	-	ND
R1564-11-c12	YES	YES	ND	+

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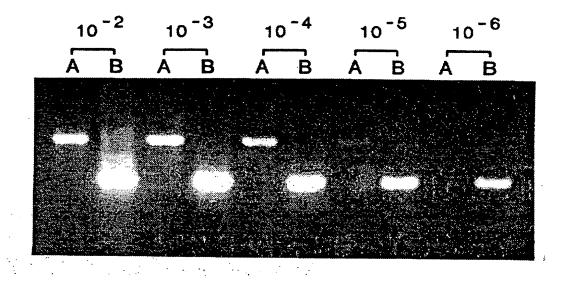






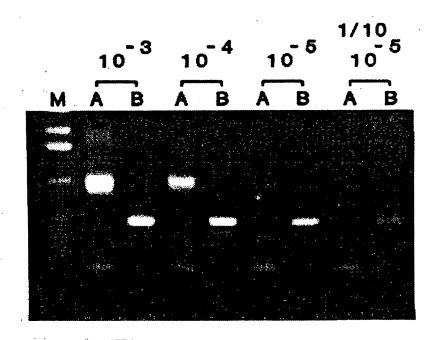
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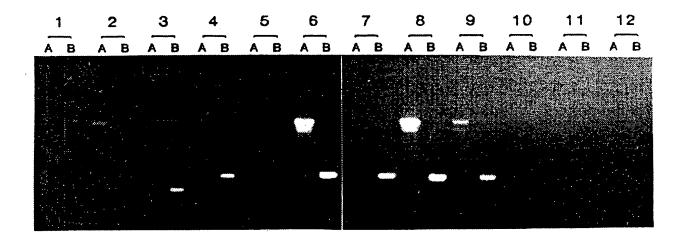


PCT/US93/10624

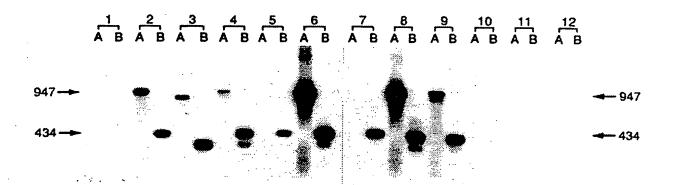
45/48

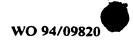


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Patient	Stage	Treatment	PSA	PAP	PSA-PCR	PSM-PCR	
1	T2NxMo	None	8.9	0.7	_	+	
2	T2NoMo	RRP 7/93	6.1	_		+	
3	T2CNoMo	PLND 5/93	4.5	0.1	-	+	
4	T2BNoMo	RRP 3/92	NMA	0.4	_	+	
5	T3NxMo	Proscar + Flutamide	51.3	1.0	-	+	
., . 6	Recur T3	I-125 1986	54.7	1.4	-	+	
7	T3ANoMo	RRP 10/92	NMA	0.3	_	+	
8	ТЗМхМо	XRT 1987	7.5	0.1	_	-	
9	T3NxMo	Proscar + Flutamide	35.4	0.7	-	-	
10	D2	S/P XRT Flutamide +Emcyt	311	4.5	` +	+	
11	D2	RRP 4/91 Lupron 10/92 Velban + Emcyt 12/92	1534	1.4	+	+	
12	T2NoMo	RRP 8/91	NMA	0.5	_	+	
13	ТЗМоМо	RRP 1/88 Lupron + Flutamide 5/92	0.1	0.3	-	-	
14	D1	PLND 1989 XRT 1989	1.6	0.4	-	_	
15	D1	Proscar + Flutamide	20.8	0.5	-		
16	T2CNoMo	RRP 4/92	0.1	0.3		-	
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